CRF ~~Errors~~ Corrected by the STIC System Branch

Serial Numb r: 10 088 594A

Processing Date: 7/22/02
Edited by: ___DC___
Verified by: ___DC___ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____ ~~ENTERED~~

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☑ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
1
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☑ Inserted mandatory headings, specifically: <2207 in Seq. 3 _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn.bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: Th above corr ctions must b communicated to th applicant in the first Offic Action. DO NOT s nd a copy of this form.

3/1/95

PCT10

RAW SEQUENCE LISTING   DATE: 07/22/2002
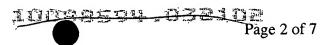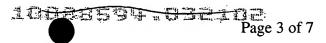PATENT APPLICATION: US/10/088,594A   TIME: 14:12:56

          Input Set : A:\PTO.DC.txt
          Output Set: N:\CRF3\07222002\J088594A.raw

        2 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
W-->   3 <120> TITLE OF INVENTION: Novel Transaldolase
W-->   4 <130> FILE REFERENCE: 00005.001198
W-->   5 <140> CURRENT APPLICATION NUMBER: US/10/088,594A
C-->   6 <141> CURRENT FILING DATE: 2002-06-11
        7 <150> PRIOR APPLICATION NUMBER: JP 99/266548
        8 <151> PRIOR FILING DATE: 1999-09-21
W-->   9 <160> NUMBER OF SEQ ID: 3
       10 <170> SOFTWARE: PatentIn Ver. 2.0
W-->   11 <210> SEQ ID NO: 1
       12 <211> LENGTH: 1080
       13 <212> TYPE: DNA
       14 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
W-->   15 <400> SEQUENCE: 1
       16 atg tct cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc   48
       17 Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
       18 1   5   10   15
       19 gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt   96
       20 Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
       21   20   25   30
       22 att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc   144
       23 Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
       24   35   40   45
       25 gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag   192
       26 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
       27   50   55   60
       28 ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc   240
       29 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
       30 65   70   75   80
       31 atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag   288
       32 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
       33   85   90   95
       34 tcc tcc aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt   336
       35 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
       36   100   105   110
       37 atc tct gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg   384
       38 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
       39   115   120   125
       40 gca aag gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca   432
       41 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
       42   130   135   140
       43 ggt tct ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt   480
       44 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val

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Output Set: N:\CRF3\07222002\J088594A.raw

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45 145                  150                  155                  160
46 aac gtc acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct    528
47 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
48                 165                  170                  175
49 gcg tac atc gag gga atc aag cag gca gct gca aac ggc cac gac gta    576
50 Ala Tyr Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
51                 180                  185                  190
52 tcc aag atc cac tct gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt    624
53 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
54                 195                  200                  205
55 gag atc gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct    672
56 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
57     210                  215                  220
58 ctg cgc ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg    720
59 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
60 225                  230                  235                  240
61 tac aag gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act    768
62 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
63                 245                  250                  255
64 cag cgc cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct    816
65 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
66                 260                  265                  270
67 gca act ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc    864
68 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
69     275                  280                  285
70 atg cca gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac    912
71 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His
72 290                  295                  300
73 ggt gac acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc    960
74 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
75 305                  310                  315                  320
76 cag ctt gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg   1008
77 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
78                 325                  330                  335
79 gag acc gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt   1056
80 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
81                 340                  345                  350
82 gag tcc atg gaa gct cgc ctg aag                                   1080
83 Glu Ser Met Glu Ala Arg Leu Lys
84          355                  360
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 1080
87 <212> TYPE: DNA
88 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
89 <400> SEQUENCE: 2
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91 cgcgagcgca ttacttccgg caatctcagc caggttattg aggaaaagtc tgtagtcggt 120
92 gtcaccacca acccagctat tttcgcagca gcaatgtcca agggcgattc ctacgacgct 180
93 cagatcgcag agctcaaggc cgctggcgca tctgttgacc aggctgttta cgccatgagc 240
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W--> (line 89)

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Output Set: N:\CRF3\07222002\J088594A.raw


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 94 atcgacgatg ttcgcaatgc ttgtgatctg ttcaccggca tcttcgagtc ctccaacggc 300
 95 tacgacggcc gcgtgtccat cgaggttgac ccacgtatct ctgctgaccg cgacgcaacc 360
 96 ctggctcagg ccaaggagct gtgggcaaag gttgatcgtc caaacgtcat gatcaagatc 420
 97 cctgcaaccc caggttcttt gccagcaatc accgacgctt ggctgagggg catcagcgtt 480
 98 aacgtcacct tgatcttctc cgttgctcgc taccgcgagg tcatcgctgc gtacatcgag 540
 99 ggaatcaagc aggcagctgc aaacggccac gacgtatcca agatccactc tgtggcttcc 600
100 ttcttcgtct cccgcgtcga cgttgagatc gacaagcgcc tcgaggcaat cggatccgat 660
101 gaggctttgg ctctgcgcgg caaggcaggc gttgccaacg ctcagcgcgc ttacgctgtg 720
102 tacaaggagc ttttcgacgc cgccgagctg cctgaaggtg ccaacactca gcgcccactg 780
103 tgggcatcca ccggcgtgaa gaaccctgcg tacgctgcaa ctctttacgt ttccgagctg 840
104 gctggtccaa acaccgtcaa caccatgcca gaaggcacca tcgacgctgt tctggaactg 900
105 ggcaacctgc acggtgacac cctgtccaac tccgcggcag aagctgacgc tgtgttctcc 960
106 cagcttgagg ctctgggcgt tgacttggca gatgtcttcc aggtcctgga gaccgagggt 1020
107 gtggacaagt ttgttgcttc ttggagcgaa ctgcttgagt ccatggaagc tcgcctgaag 1080
108 <210> SEQ ID NO: 3
109 <211> LENGTH: 4108
110 <212> TYPE: DNA
111 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
113 <220> FEATURE:
114 <221> NAME/KEY: CDS
115 <222> LOCATION: (373)..(2472)
117 <220> FEATURE:
118 <221> NAME/KEY: CDS
119 <222> LOCATION: (2643)..(3722)
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W--> 120 <400> SEQUENCE: 3

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121 tcgagagttt gaaggggtcc gattcgttcc gttcgtgacg ctttgtgagg ttttttgacg 60
122 ttgcaccgta ttgcttgccg aacatttttc ttttcctttc ggttttttcga gaattttcac 120
123 ctacaaaagc ccacgtcaca gctcccagac ttaagattgg tcacaccttt gacacatttg 180
124 aaccacagtt ggttataaaa tgggttcaac atcactatgg ttagaggtgt tgacgggtca 240
125 gattaagcaa agactacttt cggggtagat caccttttgcc aaatttgaat caattaacct 300
126 aagtcgtaga tctgatcatc ggatctaacg aaaacgaacc aaaactttgg tcccggttta 360
127 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
128            Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
129             1               5                  10
130 act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct    459
131 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
132      15              20                  25
133 gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc    507
134 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
135 30              35                  40                  45
136 tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc    555
137 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
138              50                  55                  60
139 ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca    603
140 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
141          65                  70                  75
142 ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag    651
143 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
144      80                  85                  90
```

```
145 tac atc cag ctt tac ttg ggt gga ttc ggc ctt gag atg gat gac ctg    699
146 Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu
147     95                      100                 105
148 aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac    747
149 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
150 110                     115                 120                 125
151 cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt    795
152 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
153                     130                 135                 140
154 ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc    843
155 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
156                 145                 150                 155
157 cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac    891
158 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
159             160                 165                 170
160 atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct    939
161 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
162     175                 180                 185
163 gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtg    987
164 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
165 190                 195                 200                 205
166 ttc tgg gat gac aac cgc atc tcc atc gaa gac aac act gag atc gct   1035
167 Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala
168                 210                 215                 220
169 ttc aac gag gac gtt gtt gct cgt tac aag gct tac ggc tgg cag acc   1083
170 Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr
171             225                 230                 235
172 att gag gtt gag gct ggc gag gac gtt gca gca atc gaa gct gca gtg   1131
173 Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val
174             240                 245                 250
175 gct gag gct aag aag gac acc aag cga cct acc ttc atc cgc gtt cgc   1179
176 Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg
177     255                 260                 265
178 acc atc atc ggc ttc cca gct cca acc atg atg aac acc ggt gct gtg   1227
179 Thr Ile Ile Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val
180 270                 275                 280                 285
181 cac ggt gct gct ctt ggc gca gct gag gtt gca gca acc aag act gag   1275
182 His Gly Ala Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu
183                 290                 295                 300
184 ctt gga ttc gat cct gag gct cac ttc gcg atc gac gat gag gtt atc   1323
185 Leu Gly Phe Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile
186             305                 310                 315
187 gct cac acc cgc tcc ctc gca gag cgc gct gca cag aag aag gct gca   1371
188 Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala
189             320                 325                 330
190 tgg cag gtc aag ttc gat gag tgg gca gct gcc aac cct gag aac aag   1419
191 Trp Gln Val Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys
192     335                 340                 345
193 gct ctg ttc gat cgc ctg aac tcc cgt gag ctt cca gcg ggc tac gct   1467
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Input Set : A:\PTO.DC.txt
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194 Ala Leu Phe Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala
195 350                   355                   360                   365
196 gac gag ctc cca aca tgg gat gca gat gag aag ggc gtc gca act cgt    1515
197 Asp Glu Leu Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg
198                   370                   375                   380
199 aag gct tcc gag gct gca ctt cag gca ctg ggc aag acc ctt cct gag    1563
200 Lys Ala Ser Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu
201                   385                   390                   395
202 ctg tgg ggc ggt tcc gct gac ctc gca ggt tcc aac aac acc gtg atc    1611
203 Leu Trp Gly Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile
204             400                   405                   410
205 aag ggc tcc cct tcc ttc ggc cct gag tcc atc tcc acc gag acc tgg    1659
206 Lys Gly Ser Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp
207       415                   420                   425
208 tct gct gag cct tac ggc cgt aac ctg cac ttc ggt atc cgt gag cac    1707
209 Ser Ala Glu Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His
210 430                   435                   440                   445
211 gct atg gga tcc atc ctc aac ggc att tcc ctc cac ggt ggc acc cgc    1755
212 Ala Met Gly Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg
213                   450                   455                   460
214 cca tac ggt gga acc ttc ctc atc ttc tcc gac tac atg cgt cct gca    1803
215 Pro Tyr Gly Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala
216             465                   470                   475
217 gtt cgt ctt gca gct ctc atg gag acc gac gct tac tac gtc tgg acc    1851
218 Val Arg Leu Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr
219             480                   485                   490
220 cac gac tcc atc ggt ctg ggc gaa gat ggc cca acc cac cag cct gtt    1899
221 His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val
222       495                   500                   505
223 gaa acc ttg gct gcg ctg cgc gcc atc cca ggt ctg tcc gtc ctg cgt    1947
224 Glu Thr Leu Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg
225 510                   515                   520                   525
226 cct gca gat gcg aat gag acc gcc cag gct tgg gct gca gca ctt gag    1995
227 Pro Ala Asp Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu
228                   530                   535                   540
229 tac aag gaa ggc cct aag ggt ctt gca ctg acc cgc cag aac gtt cct    2043
230 Tyr Lys Glu Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro
231             545                   550                   555
232 gtt ctg gaa ggc acc aag gag aag gct gct gaa ggc gtt cgc cgc ggt    2091
233 Val Leu Glu Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly
234             560                   565                   570
235 ggc tac gtc ctg gtt gag ggt tcc aag gaa acc cca gat gtg atc ctc    2139
236 Gly Tyr Val Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu
237       575                   580                   585
238 atg ggc tcc ggc tcc gag gtt cag ctt gca gtt aac gct gcg aaa gct    2187
239 Met Gly Ser Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala
240 590                   595                   600                   605
241 ctg gaa gct gag ggc gtt gca gct cgc gtt gtt tca gtt cct tgc atg    2235
242 Leu Glu Ala Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met
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VERIFICATION SUMMARY   DATE: 07/22/2002
PATENT APPLICATION: US/10/088,594A   TIME: 14:12:57

Input Set : A:\PTO.DC.txt
Output Set: N:\CRF3\07222002\J088594A.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:283 W: Missing Blank Line separator, <400> field identifier
L:120 M:283 W: Missing Blank Line separator, <400> field identifier
L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3